

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Evans, Ronald M.
No, David
- (ii) TITLE OF INVENTION: HORMONE-MEDIATED METHODS FOR MODULATING
EXOCENOUS GENES IN MAMMALIAN SYSTEMS, AND
PRODUCTS RELATED THERETO

- (iii) NUMBER OF SEQUENCES: 18

- (iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Gray Cary Ware & Freidenrich LLP
- (B) STREET: 4365 Executive Drive, Suite 1600
- (C) CITY: San Diego
- (D) STATE: CA
- (E) COUNTRY: USA
- (F) ZIP: 92121-2189

- (v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

- (vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

- (vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/974,590
- (B) FILING DATE: November 19, 1997
- (C) CLASSIFICATION:

- (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Reiter, Stephen E.
- (B) REGISTRATION NUMBER: 31,192
- (C) REFERENCE/DOCKET NUMBER: SALK1520-2

- (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 619-677-1409
- (B) TELEFAX: 619-677-1465

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: both

57

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(vi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Cys Xaa Xaa Cys Xaa Xaa Asp Xaa Ala Xaa Gly Xaa Tyr Xaa Xaa Xaa
1 5 10 15

Xaa Cys Xaa Xaa Cys Lys Xaa Phe Phe Xaa Arg Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
35 40 45

Xaa Xaa Xaa Lys Xaa Xaa Arg Xaa Xaa Cys Xaa Xaa Cys Arg Xaa Xaa
50 55 60

Lys Cys Xaa Xaa Xaa Gly Met
65 70

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(vi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glu Gly Cys Lys Gly
1 5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Ser Cys Lys Val
 1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2241
- (D) OTHER INFORMATION: /product= "VgEcR"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG CCC CCC CGG ACC GAT GTC AGC CTG GCG GAC GAG CTC CAC TTA GAC 48

Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp

1 5 10 15

GGC GAG GAC GTC GCG ATG GCG CAT GGC GAC GCG CTA GAC GAT TTC GAT 96

Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp

20 25 30

CTC GAC ATC TTG GGG GAC GGG GAT TCC CCG GGT CCG GGA TTT ACC CCC 144

Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Phe Thr Pro

35 40 45

CAC GAC TCC CCC TAC GGG GGT CTG GAT ATG GGC GAC TTC GAG TTT

His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe

50 55 60

GAG CAC ATG TTT ACC GAT GGC CTT GGA ATT GAC GAG TAC GGT GGG AAG 192

Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys

65 70 75 80

CTT CTA GGT ACC TCT AGA AGC ATA TCC AAT TCT ATA TCT TCA CCT CGC 288

Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg

85 90 95

GAT GAT CTC TCG CCT TCG AGC AGC TTC AAC GGA TAC TCG GCG AAC GAA 336

Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu

100 105 110

ACC TGC GAT GCG AAC AAC ACC AAC AAC GGA CCT GCG CCA CGG CTC CAA 384

Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln

115 120 125

GAG GAG CTC TCC CTC GTT TGC GGC GAC AGG GCG TCC GGC TAC CAC TAC 432
 Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr
 130 135 140

AAC GCC CTC ACC TCT GGA TCC TCC AAG GTG TTC TTT CGA CGC AGC GTT 480
 Asn Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Arg Arg Ser Val
 145 150 155 160

ACC AAC AGC CCC GTC TAC TCC TGC AAG TTC GGG CGC GCC TGC GAA ATG 528
 Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met
 165 170 175

CAC ATG TAC ATG AGC CGA AAC TCT CAG GAC TGC CGC CCC CTC AAA AAG TCC 576
 Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys
 180 185 190

CTG CCC GTC GGT ATG CGG CGG GAA TGC GTC GTC CGG GAG AAC CAA TGT 624
 Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys
 195 200 205

CGC ATG AAC CGG CCC GAA AAC AAG GCC CAC AAC GAC AAC GAC AAA ATG 672
 Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met
 210 215 220

ACC ACT TCG CGG ACC TCT CAG CAT CCC CGG AAT GGC AGC TTG CCC TCT 720
 Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser
 225 230 235 240

GGT GGC GGC CAA GAC TTT GTT AAG AAC GAC ATT CTT GAC CTT ATG ACA 768
 Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr
 245 250 255

TGC CAG CCC CCC CAG CAT CCC ACT ATT CCC CTA CTA CCT GAT GAA ATA 816
 Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile
 260 265 270

TTG CCC AAG TGT CAA CGG CGG AAT ATA CCT TCC TTA ACG TAC AAC TAT CAG 864
 Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln
 275 280 285

TTG GCC GTT ATA TAC AAG TTA ATT TGG TAC CAG GAT GGC TAT GAG CAG 912
 Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln
 290 295 300

CCA TCT GAA GAG GAT CTC ACC CCT ATA ATG ACT CAA CCC GAT GAC AAC 960
 Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn
 305 310 315 320

GAG ACC CAA ACC GAC GTC ACC TTT CGG CAT ATA ACC GAC ATA ACC ATA 1008
 Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile
 325 330 335

CTC ACG GTC CAG TTG ATT GTT GAG TTT GCT AAA GGT CTA CCA CGG TTT 1056
 Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe
 340 345 350

ACA AAG ATA CCC CAG GAG GAC CAG ATC ACC TTA CTA AAG GCC TGG TCG 1104
 Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser
 355 360 365

TCG GAG GTC ATG ATG CTG CGT ATG GCA CGA CCC TAT GAC CAC AGC TCG 1152
 Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser
 370 375 380

GAC TCA ATA TTC TTC CGG AAT AAT AGA TCA TAT ACG CGG CAT TCT TAC 1200
 Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr
 385 390 395 400

AAA ATC CCC CGA ATC CCT CAT AAC ATT GAA GAC CTG CTC CAT TTC TGC 1248
 Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys
 405 410 415

CGC CAA ATG TTC TCG ATG AAG GTC GAC AAC GTC GAA TAC GCG CTT CTC 1296
 Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu
 420 425 430

ACT CCC ATT GTC ATC TTC TCG GAC CGG CCC CCC CTC GAG AAG CCC CAA 1344
 Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Gln Lys Ala Gln
 435 440 445

CTA GTC GAA CGG ATC CAG ACC TAC TAC ATC GAC ACC CTA CCC ATT TAT 1392
 Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr
 450 455 460

ATA CTC AAC CGC CAC TGC CGG GAC TCA ATG ACC CTC GTC TTC TAC GCA 1440
 Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala
 465 470 475 480

AAC CTC CTC TCG ATC CTC ACC GAG CTC CCT ACC CTC CGC AAC CAC AAC 1488
 Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn
 485 490 495

GCC GAG ATG TGT TTC TCA CTA AAC CTC AAA AAC CGG AAA CTC CCC AAG 1536
 Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys
 500 505 510

TTC CTC GAG GAG ATC TGG GAC GTT CAT GCG ATC CGG CCA TCG CTC CAG 1584
 Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln
 515 520 525

TCC CAC CTT CAG ATT ACC CAG GAG GAC AAC CAC GAC CCT CTC GAC CGG GCT 1632
 Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala
 530 535 540

GAG CGT ATG CGG CGA TCG GTT CGG CGG CCC ATT ACC GCC CGC ATT GAT 1680
 Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp
 545 550 555 560

TGC GAC TCT GCG TCC ACT TCG GCG CGG CGA CGC CGC CGC CAG CAT CAG 1728
 Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Cln His Gln
 565 570 575

CCT CAG CCT CAG CCC CAG CCC CAA CCA CCC TCC TCC CTG ACC CAG AAC GAT 1776
 Pro Glu Pro Gln Pro Gln Pro Gln Ser Ser Leu Thr Gln Asn Asp
 580 585 590

TCC CAG CAC CAG ACA CAG CCG CAG CTA CAA CCT CAG CTA CCA CCT CAG 1824
 Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln
 595 600 605

CTC CAA CCT CAA CTG CAA CCC CAG CTC CAA CCA CAG CTT CAG ACC CAA 1872
 Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln
 610 615 620

CTC CAG CCA CAG ATT CAA CCA CAG CCA CAG CTC CTT CCC GTC TCC CCT 1920
 Leu Gln Pro Gln Ile Gln Pro Gln Leu Leu Pro Val Ser Ala
 625 630 635 640

CCC CTG CCC GCC TCC GTC ACC GCA CCT GGT TCC TTG TCC GCG GTC ACT 1968
 Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser
 645 650 655

ACC ACC ACC GAA TAC ATG GCC GGA ACT CGG CCC ATA GCA CCC ATC ACC 2016
 Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gln Pro Ile Thr
 660 665 670

CCC GCA ACC ACC AGT ATC ACC GCT GCC GTC ACC GCT ACC TCC ACC 2064
 Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr
 675 680 685

ACA TCA CGG GTC ACC CCG ATG GGC AAC GCA CTT GCA CTC GGT GTC GGG GTC 2112
 Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val
 690 695 700

GCC CGC AAC GTC ACC ATG TAT CCG AAC GCC CAG ACC GCG ATG CCC TTC 2160
 Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu
 705 710 715 720

ATG CCT GTC CCC CTC CAT TCG CAC CAA GAG CAG CTC CCT ATC GGG GCA GTC 2208
 Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val
 725 730 735

GCG GTT AAG TCG GAG CAC TCG ACG ACT GCA TAG 2241
 Ala Val Lys Ser Glu His Ser Thr Thr Ala
 740 745

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 746 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
 1 5 10 15

Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
 20 25 30

Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
 35 40 45

His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
 50 55 60

Glu Cln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys
 65 70 75 80

Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg
 85 90 95

Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu
 100 105 110

Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Cln
 115 120 125

Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr
 130 135 140

Asn Ala Leu Thr Cys Gly Ser Cys Lys Val Ile Phe Arg Arg Ser Val
 145 150 155 160

Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met
 165 170 175

Asp Met Tyr Met Arg Arg Lys Cys Gln Cys Arg Leu Lys Lys Cys
 180 185 190

Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys
 195 200 205

Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met
 210 215 220

Thr Thr Ser Pro Ser Ser Gln His Gly Asn Gly Ser Leu Ala Ser
 225 230 235 240

Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr
 245 250 255

Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile
 260 265 270

Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln
 275 280 285

Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln
 290 295 300

Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn
 305 310 315 320

Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile
 325 330 335

Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe
 340 345 350

Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser
 355 360 365

Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser
 370 375 380

Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr
 385 390 395 400

Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys
 405 410 415

Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu
 420 425 430

Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln
 435 440 445

Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr
 450 455 460

Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala
 465 470 475 480

Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn
 485 490 495

Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys
 500 505 510

Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln
 515 520 525

Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala
 530 535 540

Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp
 545 550 555 560

Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Gln His Gln
 565 570 575

Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp
 580 585 590

Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln

595 600 605

Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln
610 615 620

Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala
625 630 635 640

Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser
645 650 655

Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr
660 665 670

Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr
675 680 685

Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val
690 695 700

Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu
705 710 715 720

Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val
725 730 735

Ala Val Lys Ser Glu His Ser Thr Thr Ala
740 745

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2241
- (D) OTHER INFORMATION: /product= "VpEcR"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATC CCC CCC CGG ACC GAT GTC AGC CTG GGG GAC GAG CTC CAC TTA GAC 48

Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp

1 5 10 15

GGC GAG GAC GTC CGG ATG CGG CAT GCC GAC GCG CTA GAC GAT TTC GAT 96

Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp

20 25 30

CTC GAC ATC TTG CGG GAC CGG GAT TCC CCC GGT CCC CGA TTT ACC CCC 144
 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
 35 40 45

CAC GAC TCC GCC CCC TAC CGG GCT CTC GAT ATC GCC GAC TTC GAG TTT 192
 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
 50 55 60

CAC GAC ATC TTT ACC GAT CCC CTT GCA ATT GAC GAC TAC CGT CGG AAC 240
 Glu Cln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Lys
 65 70 75 80

CTT CTA CGT ACC TCT AGA ACC ATA TCG AAT TCT ATA TCT TCA GGT CCC 288
 Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg
 85 90 95

GAT GAT CTC TCG CCT TCG ACC AGC TTG AAC CGA TAC TCG CGG AAC GAA 336
 Asp Asp Leu Ser Pro Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu
 100 105 110

AGC TCC CAT CGG AAC AAC ACC AAC CGA CCT CGC CCA CGG CTC CAA 384
 Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Cln
 115 120 125

GAG GAG CTC TCC CTC CTT TCC CGG GAC ACC CGC TCC CGC TAC CAC TAC 432
 Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr
 130 135 140

AAC CCC CTC ACC TGT GAG CGC TCC AAG CGG TTC TTT CGA CGG AGC GTT 480
 Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val
 145 150 155 160

ACC AAG ACC CGC CTC TAC TCC TCC AAG TTC CGG CGC CGC TCC GAA ATG 528
 Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met
 165 170 175

GAC ATG TAC ATG AGC CGA AAC TGT CAG GAC TCC CGC CTG AAA AAG TGC 576
 Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys
 180 185 190

CTC CGC GTC CGT ATC CGG CGG GAA TCC CTC GTC CGC CGG GAG AAC CAA TGT 624
 Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys
 195 200 205

GCG ATG AAG CGG CGC GAA AAC AAG CGC CAG AAC GAC AAC GAC AAA ATC 672
 Ala Met Lys Arg Arg Glu Lys Ala Gln Lys Glu Lys Asp Lys Met
 210 215 220

ACC ACT TCG CGG ACC TCT CAG CAT CGC CGG AAT CGC ACC TTC CGC TCT 720
 Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser
 225 230 235 240

GGT CGC CGC CAA GAC TTT GTT AAC AAC GAG ATT CTT GAC CTT ATG ACA 768
 Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr
 245 250 255

TGG GAG CCC CCC CAG CAT CCC ACT ATT CCG CTA CTA CCT GAT GAA ATA 816
 Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile
 260 265 270

TTC GCC AAG TGT CAA CCC CCC AAT ATA CCT TCC TTA ACC TAC AAT CAG 864
 Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln
 275 280 285

TTC CCC CTT ATA TAC AAC TTA ATT TGG TAC CAC CAT CCC TAT GAC CAC 912
 Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln
 290 295 300

CCA TCT GAA GAG GAT CTC AGG CCT ATA ATG AGT CAA CCC GAT GAC AAC 960
 Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn
 305 310 315 320

GAC ACC CAA ACC GAC GTC ACC TTT CGG CAT ATA ACC GAG ATA ACC ATA 1008
 Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile
 325 330 335

CTC ACC GTC CAG TTC ATT GTT GAG TTT CCT AAA GGT CTA CCA CCC TTT 1056
 Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Ileu Pro Ala Phe
 340 345 350

ACA AAG ATA CCC CAG GAG GAC CAC ATC ACC TTA CTA AAG GCC TCC TCG 1104
 Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser
 355 360 365

TGG GAG GTC ATG ATG CTG CGT ATG GCA CGA CCC TAT GAC CAC ACC TCG 1152
 Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser
 370 375 380

GAC TCA ATA TTC TTC CGG AAT AAT AGA TCA TAT ACC CGG GAT TTT TAC 1200
 Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr
 385 390 395 400

AAA ATG GCC GGA ATG CCT GAT AAC ATT GAA GAC CTC CTG CAT TTC TCC 1248
 Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys
 405 410 415

CCC CAA ATG TTC TCG ATG AAG GTG GAC AAC CTC GAA TAC GGC CTT CTC 1296
 Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu
 420 425 430

ACT CCC ATT GTG ATC TTC TCG GAC CGG CCC CGC CTG CAC AAG CCC CAA 1344
 Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln
 435 440 445

CTA GTC GAA CGG ATC CAG ACC TAC TAC ATC GAC ACC CTA CGC ATT TAT 1392
 Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr
 450 455 460

ATA CTC AAC CCC CAC TGC CGG GAC TCA ATG AGC CTC GTC TTC TAC CGA 1440
 Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala
 465 470 475 480

AAG CTG CTC TCC ATC CTC ACC GAG CTC CGT ACG CTC CCC AAC CAG AAC 1488
 Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn
 485 490 495

GCC GAG ATG TGT TTC TCA CTA AAG CTC AAA AAC CGC AAA CTG CCC AAG 1536
 Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys
 500 505 510

TTC CTC GAC GAC ATC TCG GAC CTT CAT CCC ATC CCG CCA TCG CTC CAG 1584
 Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln
 515 520 525

TCG CAC CCT CAG ATT ACC CAG GAG GAC AAC GAG CGT CTC CAG CCC CCT 1632
 Ser His Leu Glu Ile Thr Glu Glu Glu Asn Glu Arg Leu Glu Arg Ala
 530 535 540

GAG CGT ATG CGG GCA TCG GTT GGG CCC ATT ACC CCC CCC ATT GAT 1680
 Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp
 545 550 555 560

TCC CAC TCT CCC TCC ACT TCG CCC CCC GCA CCC CCC CAG CAT CAG 1728
 Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Gln His Gln
 565 570 575

CCT CAG CCT CAG CCC CAG CCC CAA CCC TCC TCC CTC ACC CAG AAC GAT 1776
 Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp
 580 585 590

TCC CAG CAC CAG ACA CAG CCG CAG CTA CAA CCT CAG CTA CCA CCT CAG 1824
 Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln
 595 600 605

CTC CAA CCT CAA CTC CAA CCC CAG CTC CAA CCA CAG CTT CAG ACC CAA 1872
 Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln
 610 615 620

CTC CAG CCA CAG ATT CAA CCA CAG CCA CAG CTC CTT CCC CTC TCC CCT 1920
 Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Lep Leu Pro Val Ser Ala
 625 630 635 640

CCC GTG CCC CCC TCC GTC ACC GCA CCT GGT TCC TTG TCC GCG GTC ACT 1968
 Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser
 645 650 655

ACC AGC ACC GAA TAC ATG GCC GGA ACT CGG CCC ATA GCA CCC ATC ACC 2016
 Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr
 660 665 670

CGG GCA ACC ACC ACC ACT ATC ACC CCT GCC CTT ACC CCT ACC TCC ACC 2064
 Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr
 675 680 685

ACA TCA GCG GTC CGG AAC GGA CTT GGA GTC CCT GTT CCC CTG 2112
 Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val
 690 695 700

GGC CCC AAC GTC ACC ATG TAT CCC AAC CCC CAG ACG CCC ATG CCC TTG 2160
 Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu
 705 710 715 720

ATG CGT GTA CCC CTG CAT TCG CAC CAA CAG CAG CTT ATC GGG GGA CTC 2208
 Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val
 725 730 735

GCC CTT AAC TCG GAG CAC TCG ACC ACT GCA TAG 2241
 Ala Val Lys Ser Glu His Ser Thr Thr Ala
 740 745

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 746 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
 1 5 10 15

Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
 20 25 30

Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
 35 40 45

His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
 50 55 60

Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Lys
 65 70 75 80

Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg
 85 90 95

Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu
 100 105 110

Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln
 115 120 125

Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr
 130 135 140

Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val
 145 150 155 160

Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met

165 170 175

Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys
 180 185 190

Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys
 195 200 205

Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met
 210 215 220

Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Ileu Ala Ser
 225 230 235 240

Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr
 245 250 255

Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile
 260 265 270

Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln
 275 280 285

Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln
 290 295 300

Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn
 305 310 315 320

Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile
 325 330 335

Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe
 340 345 350

Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser
 355 360 365

Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser
 370 375 380

Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr
 385 390 395 400

Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys
 405 410 415

Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu
 420 425 430

Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln
 435 440 445

Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr
 450 455 460

Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala
 465 470 475 480

Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn
 485 490 495

Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys
 500 505 510

Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln
 515 520 525

Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala
 530 535 540

Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp
 545 550 555 560

Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Ala Gln His Gln
 565 570 575

Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp
 580 585 590

Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln
 595 600 605

Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln
 610 615 620

Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala
 625 630 635 640

Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser
 645 650 655

Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr
 660 665 670

Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr
 675 680 685

Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val
 690 695 700

Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu
 705 710 715 720

Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val
 725 730 735

Ala Val Lys Ser Glu His Ser Thr Thr Ala
 740 745

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3126
- (D) OTHER INFORMATION: /product= "GEER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATC GAC TCC AAA GAA TCA TTA ACT CCT GCT ACA GAA GAA AAC CCC ACC	48
Met Asp Ser Lys Glu Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser	
1 5 10 15	
ACT CTG CTT GCT CAG GAC AGG CGA CAT CTG ATG GAC TTC TAT AAA ACC	96
Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr	
20 25 30	
CTA AGA GGA GGA GCT ACT GTG AAG GTT TCT GCG TCT TCA CCC TCA CTG	144
Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu	
35 40 45	
GCT CTC GCT TCT CAA TCA GAC TCC AAC CAG CGA AGA CTT TTC CTT GAT	192
Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp	
50 55 60	
TTT CCA AAA CGC TCA GTA AGC AAT GGC CAG CAC CCA GAT CTC TCC AAA	240
Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys	
65 70 75 80	
GCA GTT TCA CTC TCA ATG GGA CTG TAT ATG GCA GAG ACA GAA ACA AAA	288
Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys	
85 90 95	
GTC ATG GGA AAT GAC CTG GGA TTC CCA CAG CAG GGC CAA ATC ACC CTT	336
Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gln Ile Ser Leu	
100 105 110	
TCC TCG GGG GAA ACA GAC TTA AAG GTT TTG GAA GAA ACC ATT GCA AAC	384
Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn	
115 120 125	
CTC AAT AGC TCG ACC ACT GTT CCA GAG AAC CCC AAC ACT TCA GCA TCC	432
Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser	
130 135 140	

ACT CCT GTG TCT CCT CCC CCC ACA GAC AAG GAG TTT CCA AAA ACT CAC 480
 Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His
 145 150 155 160

TCT GAT GTA TCT TCA GAA CAG CAA CAT TTC AAC GGC CAG ACT GGC ACC 528
 Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr
 165 170 175

AAC CCT GCC AAT GTG AAA TTG TAT ACC ACA GAC CAA ACC ACC TTT GAC 576
 Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp
 180 185 190

ATT TTG CAG GAT TTG GAC TTT CCT TCT CCC CCA CGT AAA GAG ACC 624
 Ile Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr
 195 200 205

AAT GAG AGT CCT TGG AGA TCA GAC CTC TTG ATA GAT GAA AAC TGT TTG 672
 Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu
 210 215 220

CTT TCT CCT CTG CCC CGA GAA GAC GAT TCA TTC CTT TTG CAA GGA AAC 720
 Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn
 225 230 235 240

TCG AAT GAG GAC TGC AAG CCT CTC ATT TTA CCG GAC ACT AAA CCC AAA 768
 Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys
 245 250 255

ATT AAG GAT AAT GGA GAT CTC GTT TTG TCA ACC CCC AGT AAT GTA ACA 816
 Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr
 260 265 270

CTC CCC CAA GTG AAA ACA GAA AAA GAA GAT TTC ATC GAA CTC TGC ACC 864
 Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr
 275 280 285

CCT CCC GTA ATT AAC CAA GAG AAA CTG CCC ACA CCTT TAC TGT CAG GCA 912
 Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Lys Gln Ala
 290 295 300

AGC TTT CCT GCA GCA AAT ATA ATT GGT AAT AAA ATC TCT GCC ATT TCT 960
 Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser
 305 310 315 320

GTT CAT GCT GTG ACT ACC TCT GCA GGA CAG ATG TAC CAC TAT GAC ATG 1008
 Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met
 325 330 335

AAT ACA GCA TCC CTT TCT CAA CAC CAG GAT CAG AAC CCT ATT TTT AAT 1056
 Asn Thr Ala Ser Leu Ser Gln Gln Asp Gln Lys Pro Ile Phe Asn
 340 345 350

GTC ATT CCA CCA ATT CCC GTT GGT TCC GAA AAT TGG AAT AGG TGC CAA 1104
 Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp Asn Arg Cys Gln
 355 360 365

GCA TCT CGA GAT GAC AAC TTG ACT TCT CTC GGG ACT CTC AAC TTG CCT 1152
 Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro
 370 375 380

GGT CGA ACA GTT TTT TCT AAT GCC TAT TCA AGC CCC AGC ATG AGA CCA 1200
 Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro
 385 390 395 400

GAT GTA ACC TCT CCT CCA TCC AGC TCC TCA ACA GCA ACA ACA GGA CCA 1248
 Asp Val Ser Ser Pro Pro Ser Ser Ser Thr Ala Thr Thr Gly Pro
 405 410 415

CCT CCC ACC GGC CCC CTC CAA GAG GAC CTC TCC CTC CTT TGC GGC GAC 1296
 Pro Pro Ser Gly Arg Val Gln Glu Glu Leu Cys Leu Val Cys Gly Asp
 420 425 430

AGG CCC TCC GGC TAC CAC TAC AAC GCC CTC ACC TCT CGA TCC TGC AAC 1344
 Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Gly Ser Cys Lys
 435 440 445

GTG TTC TTT CGA CGC AGC GTT ACG AAG ACC GGC GTC TAC TGC TGC AAG 1392
 Val Phe Phe Arg Arg Ser Val Thr Lys Ser Ala Val Tyr Cys Cys Lys
 450 455 460

TTC CGG CGC CCC TCC GAA ATC CAC ATC TAC ATC AGG CGA AAC TCT CAG 1440
 Phe Gly Arg Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys Cys Gln
 465 470 475 480

GAC TCC CGG CTC AAA AAC TCC CTG GCC CTG GGT ATG CGG CGG GAA TCC 1488
 Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro Glu Cys
 485 490 495

GTC GTC CGG GAC AAC CAA TGT CGG ATG AAG CGG CGC GAA AAC AAG CGC 1536
 Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Arg Glu Lys Lys Ala
 500 505 510

CAC AAC GAC AAC GAC AAA ATC ACC ACT TCG CGG ACC TCT CAG CAT GGC 1584
 Gln Lys Glu Lys Asp Lys Met Thr Thr Ser Pro Ser Ser Gln His Gly
 515 520 525

CGC AAT CGG AGC TTG CGC TCT CGT CGG CGG CAA GAC TTT CGT AAC AAC 1632
 Gly Asn Gly Ser Leu Ala Ser Gly Gly Gln Asp Phe Val Lys Lys
 530 535 540

GAG ATT CTT GAC CTT ATG ACA TGC GAG CGG CGC CAG CAT GCC ACT ATT 1680
 Glu Ile Leu Asp Leu Met Thr Cys Glu Pro Pro Gln His Ala Thr Ile
 545 550 555 560

CCC CTA CTA CCT GAT GAA ATA TTG CGC AAG TCT CAA CGG CGC AAT ATA 1728
 Pro Leu Leu Pro Asp Glu Ile Leu Ala Lys Cys Gln Ala Arg Asn Ile
 565 570 575

CCT TCC TTA ACC TAC AAT CAG TTG CGC GTT ATA TAC AAG TTA ATT CGC 1776
 Pro Ser Leu Thr Tyr Asn Gln Leu Ala Val Ile Tyr Lys Leu Ile Trp
 580 585 590

TAC CAG GAT CCC TAT GAG CAG CCA TCT GAA GAG GAT CTC AGG CGT ATA 1824
 Tyr Gln Asp Gly Tyr Glu Gin Pro Ser Glu Glu Asp Leu Arg Arg Ile
 595 600 605

ATG ACT CAA CCC GAT GAG AAC GAG CAA ACC GAC GTC AGC TTT CCG 1872
 Met Ser Gin Pro Asp Glu Asn Glu Ser Gin Thr Asp Val Ser Phe Arg
 610 615 620

CAT ATA ACC GAG ATA ACC ATA CTC ACG GTC CAG TTC ATT GTT GAG TTT 1920
 His Ile Thr Glu Ile Thr Ile Leu Thr Val Gin Leu Ile Val Glu Phe
 625 630 635 640

GCT AAA GGT CTA CCA CGC TTT ACA AAC ATA CCC CAG GAC GAC CAG ATC 1968
 Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gin Glu Asp Gln Ile
 645 650 655

ACG TTA CTA AAC GCC TCC TCG TCG GAC GTC ATC ATC CTC CGT ATG GCA 2016
 Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Met Ala
 660 665 670

CGA CGC TAT GAC CAC ACC TCG GAC TCA ATA TTC TTC CGG AAT AAT ACA 2064
 Arg Arg Tyr Asp His Ser Ser Asp Ser Ile Phe Phe Ala Asn Asn Arg
 675 680 685

TCA TAT ACC CGG GAT TCT TAC AAA ATC CCC GGA ATG GCT GAT AAC ATT 2112
 Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp Asn Ile
 690 695 700

GAA GAC CTG CTG CAT TTC TCC CGC CAA ATG TTC TCC ATC AAC GTC GAC 2160
 Glu Asp Leu Leu His Phe Cys Arg Gln Met Phe Ser Met Lys Val Asp
 705 710 715 720

AAC GTC GAA TAC CGG CTT CTC ACT GCC ATT GTG ATC TTC TCG GAC CGG 2208
 Asn Val Glu Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg
 725 730 735

CCC CGC CTG GAC AAG CCC CAA CTA CTC GAA CGC ATC CAG ACC TAC TAC 2256
 Pro Gly Leu Glu Lys Ala Gln Leu Val Glu Ala Ile Gln Ser Tyr Tyr
 740 745 750

ATC GAC ACC CTA CCC ATT TAT ATA CTC AAC CCC CAC TGC CGC GAC TCA 2304
 Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg His Cys Gly Asp Ser
 755 760 765

ATC AGC CTC GTC TTC TAC GCA AAG CTG CTC TCG ATC CTC ACC GAG CTG 2352
 Met Ser Leu Val Phe Tyr Ala Lys Leu Leu Ser Ile Leu Thr Glu Leu
 770 775 780

GCT ACC CTC CGC AAC CAG AAC CCC GAG ATC TCT TTC TCA CTA AAG CTC 2400
 Arg Thr Leu Gly Asn Gln Asn Ala Glu Met Cys Phe Ser Leu Lys Leu
 785 790 795 800

AAA AAC CCC AAA CTC CCC AAC GTC GAC GAG ATC TGG GAC CTT CAT 2448
 Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu Ile Trp Asp Val His
 805 810 815

CCC ATC CCG CCA TCG GTC CAG TCG CAC CTT CAG ATT ACC CAC CAG GAG | 2496
 Ala Ile Pro Pro Ser Val Gln Ser His Leu Gln Ile Thr Gln Glu Glu
 820 825 830

AAC GAG CGT CTC CAC CGG CCT GAG CGT ATG CGG GCA TCG GTT GGG CCC | 2544
 Asn Glu Arg Leu Glu Arg Ala Glu Arg Met Arg Ala Ser Val Gly Gly
 835 840 845

GCC ATT ACC CCC CCC ATT GAT TGC GAC TCT GCG TCC ACT TCC CCC CCC | 2592
 Ala Ile Thr Ala Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala
 850 855 860

GCA CCC CCC CCC CAG CAT CAG CCT CAG CCT CAG CCC CAA CCC CAA CCC | 2640
 Ala Ala Ala Ala Gln His Gln Pro Gln Pro Gln Pro Gln Pro
 865 870 875 880

TCC TCC CTG ACC CAG AAC GAT TCC CAG CAC CAG ACA CAG CCC CAG CTA | 2688
 Ser Ser Leu Thr Gln Asn Asp Ser Gln His Gln Thr Gln Pro Gln Leu
 885 890 895

CAA CCT CAG CTA CCA CCT CAG CTC CAA GGT CAA CTG CAA CCC CAG CTC | 2736
 Gln Pro Gln Leu Pro Pro Gln Leu Gln Gly Gln Leu Gln Pro Gln Leu
 900 905 910

CAA CCA CAG CTT CAG ACC CAA CTC CAG CCA CAG ATT CAA CCA CAG CCA | 2784
 Gln Pro Gln Leu Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro
 915 920 925

CAG CTC CTT CCC GTC TCC CCT CCC CTC CCC CCC TCC GTC ACC GCA CCT | 2832
 Gln Leu Leu Pro Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro
 930 935 940

GGT TCC TTG TCC GCG GTC ACT ACC ACC AGC GAA TAC ATG GGC GGA ACT | 2880
 Gly Ser Leu Ser Ala Val Ser Thr Ser Ser Glu Tyr Met Gly Gly Ser
 945 950 955 960

CCC CCC ATA CGA CCC ATC ACC CCG CCA ACC ACC ACC ACT ATC ACC CCT | 2928
 Ala Ala Ile Gly Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala
 965 970 975

CCC GTT ACC CCT ACC TCC ACC ACA TCA CGG GTC CCC ATG GGC AAC GGA | 2976
 Ala Val Thr Ala Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly
 980 985 990

GTT GGA GTC GGT GTT GGG GTC GGC GGC AAC GTC ACC ATG TAT GCG AAC | 3024
 Val Gly Val Gly Val Gly Gly Asn Val Ser Met Tyr Ala Asn
 995 1000 1005

CCC CAC ACC CCC ATC CCC TTG ATG CCT GTC CCC CTC CAT TCG CAC CAA | 3072
 Ala Gln Thr Ala Met Ala Leu Met Gly Val Ala Leu His Ser His Gln
 1010 1015 1020

CAC CAG CTT ATC CCC CCA GTC CCC CCT AAC TCG CAG CAC TCG ACC ACT | 3120
 Glu Gln Leu Ile Gly Gly Val Ala Val Lys Ser Glu His Ser Thr Thr
 1025 1030 1035 1040

GCA TAG
Ala

3126

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1041 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Asp Ser Lys Glu Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser
 1 5 10 15

Ser Val Leu Ala Cln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr
 20 25 30

Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
 35 40 45

Ala Val Ala Ser Cln Ser Asp Ser Lys Cln Arg Arg Leu Leu Val Asp
 50 55 60

Phe Pro Lys Gly Ser Val Ser Asn Ala Cln Cln Pro Asp Leu Ser Lys
 65 70 75 80

Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
 85 90 95

Val Met Gly Asn Asp Leu Gly Phe Pro Cln Cln Gln Ile Ser Leu
 100 105 110

Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn
 115 120 125

Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser
 130 135 140

Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His
 145 150 155 160

Ser Asp Val Ser Ser Glu Cln Cln His Leu Lys Gly Cln Thr Gly Thr
 165 170 175

Asn Gly Gly Asn Val Lys Leu Tyr Thr Asp Gln Ser Thr Phe Asp
 180 185 90

Ile Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr
 195 200 205

Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu
 210 215 220

Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn
 225 230 235 240

Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys
 245 250 255

Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr
 260 265 270

Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Ileu Cys Thr
 275 280 285

Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala
 290 295 300

Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser
 305 310 315 320

Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met
 325 330 335

Asn Thr Ala Ser Leu Ser Gln Gln Gln Asp Gln Lys Pro Ile Phe Asn
 340 345 350

Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp Asn Arg Cys Gln
 355 360 365

Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro
 370 375 380

Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro
 385 390 395 400

Asp Val Ser Ser Pro Pro Ser Ser Ser Thr Ala Thr Thr Gly Pro
 405 410 415

Pro Pro Ser Gly Arg Val Gln Glu Glu Leu Cys Leu Val Cys Gly Asp
 420 425 430

Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Gly Ser Cys Lys
 435 440 445

Val Phe Phe Arg Arg Ser Val Thr Lys Ser Ala Val Tyr Cys Cys Lys
 450 455 460

Phe Gly Arg Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys Cys Gln
 465 470 475 480

Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro Glu Cys
 485 490 495

Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Arg Glu Lys Ala
 500 505 510

Gln Lys Glu Lys Asp Lys Met Thr Thr Ser Pro Ser Ser Gln His Gly
 515 520 525

Gly Asn Gly Ser Leu Ala Ser Gly Gly Gln Asp Phe Val Lys Lys
 530 535 540

Glu Ile Leu Asp Leu Met Thr Cys Glu Pro Pro Gln His Ala Thr Ile
 545 550 555 560

Pro Leu Leu Pro Asp Glu Ile Leu Ala Lys Cys Gln Ala Arg Asn Ile
 565 570 575

Pro Ser Leu Thr Tyr Asn Gln Leu Ala Val Ile Tyr Lys Leu Ile Trp
 580 585 590

Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Arg Arg Ile
 595 600 605

Met Ser Gln Pro Asp Glu Asn Glu Ser Glu Thr Asp Val Ser Phe Arg
 610 615 620

His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe
 625 630 635 640

Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln Glu Asp Gln Ile
 645 650 655

Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Met Ala
 660 665 670

Arg Arg Tyr Asp His Ser Ser Asp Ser Ile Phe Phe Ala Asn Asn Arg
 675 680 685

Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp Asn Ile
 690 695 700

Glu Asp Leu Leu His Phe Cys Arg Gln Met Phe Ser Met Lys Val Asp
 705 710 715 720

Asn Val Glu Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg
 725 730 735

Pro Gly Leu Glu Lys Ala Gln Leu Val Glu Ala Ile Gln Ser Tyr Tyr
 740 745 750

Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg His Cys Gly Asp Ser
 755 760 765

Met Ser Leu Val Phe Tyr Ala Lys Leu Leu Ser Ile Leu Thr Glu Leu
 770 775 780

Arg Thr Leu Gly Asn Gln Asn Ala Glu Met Cys Phe Ser Leu Lys Leu
 785 790 795 800

Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu Ile Trp Asp Val His
 805 810 815

Ala Ile Pro Pro Ser Val Gln Ser His Leu Gln Ile Thr Gln Glu Glu
 820 825 830

Asn Glu Arg Leu Glu Arg Ala Glu Arg Met Arg Ala Ser Val Gly Gly
 835 840 845

Ala Ile Thr Ala Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala
 850 855 860

Ala Ala Ala Ala Gln His Gln Pro Gln Pro Gln Pro Gln Pro Gln Pro
 865 870 875 880

Ser Ser Leu Thr Gln Asn Asp Ser Gln His Gln Thr Gln Pro Gln Leu
 885 890 895

Gln Pro Gln Leu Pro Pro Gln Leu Gln Gly Gln Leu Gln Pro Gln Leu
 900 905 910

Gln Pro Gln Leu Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro
 915 920 925

Gln Leu Leu Pro Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro
 930 935 940

Gly Ser Leu Ser Ala Val Ser Thr Ser Ser Glu Tyr Met Gly Gly Ser
 945 950 955 960

Ala Ala Ile Gly Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala
 965 970 975

Ala Val Thr Ala Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly
 980 985 990

Val Gly Val Gly Val Gly Val Gly Gly Asn Val Ser Met Tyr Ala Asn
 995 1000 1005

Ala Gln Thr Ala Met Ala Leu Met Gly Val Ala Leu His Ser His Gln
 1010 1015 1020

Glu Gln Leu Ile Gly Gly Val Ala Val Lys Ser Glu His Ser Thr Thr
 1025 1030 1035 1040

Ala

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(iii) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product = "Modified Ecdysone Response Element"
/note = "N at position 7 is 0 up to 5 nucleotides,
with 1 nucleotide being especially preferred."

(iv) SEQUENCE DESCRIPTION: SEQ ID NO:10:

RGBNNMNTGN NCY

13

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(iii) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product = "Modified Ecdysone Response Element"
/note = "N at position 7 can be 0 up to 5
nucleotides, with 1 nucleotide being preferred."

(iv) SEQUENCE DESCRIPTION: SEQ ID NO:11:

RGNNCAKNN VCY

13

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ACTGCCATCTCTCT

13

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "Ecdysone Response Element"
/note = "N at position 7 can be 0 up to 5 nucleotides, with 3 nucleotides being preferred."

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:13:

RGBNNNNRGNMNM

13

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TACAACCCCC TCACCTGTGG ATCCCTCCAAG CTCTTTCTTT CGACCCAGC

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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTACTCCCCG CGCCGGGGCTA TCGGGGGGGG GGCTAATGCC TAGGGGGGGG GCA 53

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTACTGCCCG CGCCCTACCG ATTAGCCCC CCCGGATAC CCCCCCCCCC GCA 53

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGCTCGATGG ACAAGTGCAT ATGTTCTTTGC TGAA 34

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION/SEQ ID NO:18:

ACCTTTCAGC AACACAACAA TGCACTTGTC CATCG

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